

SEQUENCE LISTING

<110> Chadwick, Brian Paul
Frischauf, Anna-Maria

<120> METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
POLYPEPTIDES AND NUCLEIC ACIDS

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<140> 09/240,639
<141> 1999-01-29

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<170> PatentIn Ver. 2.0

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 Arg Glu Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro
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 Gly Leu Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile
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 Arg Glu Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp
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Ile Lys Gly Pro Phe Val Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser			
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 Ser Pro Leu Ile Arg Leu Pro Ile Glu Pro Pro Val Phe Val Gly Thr
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Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro Gln Asp Val Pro Arg Ala
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Phe Glu Glu Cys Met Gln Lys Val Lys Gly Gln Val Pro Ser His Leu
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His Gly Ser Thr Pro Ile His Leu Gly Ala Thr Ala Gly Met Arg Leu
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Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp Phe Arg Gly Ala Gln Ile
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Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly Trp Ile Thr Ala Asn Tyr
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Leu Met Gly Asn Phe Leu Glu Lys Asn Leu Trp His Met Trp Val His
195 200 205

Pro His Gly Val Glu Thr Thr Gly Ala Leu Asp Leu Gly Gly Ala Ser
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Thr Gln Ile Ser Phe Val Ala Gly Glu Lys Met Asp Leu Asn Thr Ser
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Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr Val Tyr Thr Leu Tyr Thr
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His Ser Phe Gln Cys Tyr Gly Arg Asn Glu Ala Glu Lys Lys Phe Leu
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Ala Met Leu Leu Gln Asn Ser Pro Thr Lys Asn His Leu Thr Asn Pro
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Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe Thr Met Gly His Val Phe
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His Val Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu
65 70 75

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gcc aaa gac tca atc ccc cga agt cac tgg aaa aag acc cca gtg gtc		624
Ala Lys Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val		
115	120	125
cta aag gca aca gca gga cta cgc tta ctg cca gaa cac aaa gcc aag		672
Leu Lys Ala Thr Ala Gly Leu Arg Leu Pro Glu His Lys Ala Lys		
130	135	140
gct ctg ctc ttt gag gta aag gag atc ttc agg aag tca cct ttc ctg		720
Ala Leu Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu		
145	150	155
gta cca aag ggc agt gtt agc atc atg gat gga tcc gac gaa ggc ata		768
Val Pro Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile		
160	165	170
tta gct tgg gtt act gtg aat ttt ctg aca ggt cag ctg cat ggc cac		816
Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His		
175	180	185
190		
aga cag gag act gtg ggg acc ttg gac cta ggg gga gcc tcc acc caa		864
Arg Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln		
195	200	205
atc acg ttc ctg ccc cag ttt gag aaa act ctg gaa caa act cct agg		912
Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg		
210	215	220
ggc tac ctc act tcc ttt gag atg ttt aac agc act tat aag ctc tat		960
Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr		
225	230	235
aca cat agt tac ttg gga ttt gga ttg aaa gct gca aga cta gca acc		1008
Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr		
240	245	250
ctg gga gcc ctg gag aca gaa ggg act gat ggg cac act ttc cgg agt		1056
Leu Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser		
255	260	265
270		
gcc tgt tta ccg aga tgg ttg gaa gca gag tgg atc ttt ggg ggt gtg		1104
Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val		
275	280	285
aaa tac cag tat ggt ggc aac caa gaa ggg gag gtg ggc ttt gag ccc		1152
Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro		
290	295	300
tgc tat gcc gaa gtg ctg agg gtg gta cga gga aaa ctt cac cag cca		1200
Cys Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro		
305	310	315
gag gag gtc cag aga ggt tcc ttc tat gct ttc tct tac tat tat gac		1248
Glu Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp		
320	325	330

cga gct gtt gac aca gac atg att gat tat gaa aag ggg ggt att tta		1296
Arg Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu		
335	340	345
350		
aaa gtt gaa gat ttt gaa aga aaa gcc agg gaa gtg tgt gat aac ttg		1344
Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu		
355	360	365
gaa aac ttc acc tca ggc agt cct ttc ctg tgc atg gat ctc agc tac		1392
Glu Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr		
370	375	380
atc aca gcc ctg tta aag gat ggc ttt ggc ttt gca gac agc aca gtc		1440
Ile Thr Ala Leu Leu Lys Asp Gly Phe Ala Asp Ser Thr Val		
385	390	395
tta cag ctc aca aag aaa gtg aac aac ata gag acg ggc tgg gcc ttg		1488
Leu Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu		
400	405	410
ggg gcc acc ttt cac ctg ttg cag tct ctg ggc atc tcc cat		1530
Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His		
415	420	425
tgaggccacg tactccttg gagacctgca tttgccaaca ccttttaag gggaggagag		1590
agcacttagt ttctgaacta gtctggaca tcctggactt gagcctagag atttaggttt		1650
aattaatttt acacatctaa tgtgaactgc tgcctaacca ctcaagagta cacagctggc		1710
accagagcat cacagagagc cctgtgagcc aaaaagtata gtttggAAC ttaaccttgg		1770
agtgagagcc cagggacagg tccctggaaa ccaaagaaaa atcgatttc aacccttga		1830
gtgcctcatt ccactgaata tttaaatttt cctcttaaat ggtaaactga cttattgcaa		1890
tcccaagacc catcaatatc agtattttt tcctccctat acagtgcctt gcccaccctt		1950
atctgcaccc acctccccctg aaaaagagag aaaaaaaaaa aaaaaaaaa		1998

<210> 6
<211> 428
<212> PRT
<213> Homo sapiens

<400> 6			
Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys			
1	5	10	15
Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly			
20	25	30	
Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu			
35	40	45	
Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val			
50	55	60	

Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
65 70 75 80

Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
85 90 95

Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
100 105 110

Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
115 120 125

Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
130 135 140

Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
145 150 155 160

Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala
165 170 175

Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
180 185 190

Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
195 200 205

Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
210 215 220

Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
225 230 235 240

Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
245 250 255

Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
260 265 270

Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr
275 280 285

Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
290 295 300

Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu
305 310 315 320

Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
325 330 335

Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val
340 345 350

Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
355 360 365

Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
370 375 380

Ala Leu Leu Lys Asp Gly Phe Gly Ala Asp Ser Thr Val Leu Gln
385 390 395 400

Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala
405 410 415

Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
420 425

<210> 7
<211> 2119
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (205)..(1599)

<400> 7
acgttgacac aggaatgaag agtgtattgg ctgaatcttc aagcagaggc gatattgacc 60
atgtgcttt taaattggcc tgcgtgaccc gcccacttgg tgtaaaagaa gaaccggcca 120
aagggagggc ctgaaggacc tccacaggag tgtgagcagc actgcttcag caacaaagcc 180
tcaggtccac atcttggaa gaat atg gcc act tcc tgg ggg gct gtc ttc 231
Met Ala Thr Ser Trp Gly Ala Val Phe
1 5

atg ctg atc ata gcc tgc gtt ggc agc act gtc ttc tac aga gaa cag 279
Met Leu Ile Ile Ala Cys Val Gly Ser Thr Val Phe Tyr Arg Glu Gln
10 15 20 25

cag acc tgg ttt gaa ggt gtc ttc ttg tct tcc atg tgc ccc att aat 327
Gln Thr Trp Phe Glu Gly Val Phe Leu Ser Ser Met Cys Pro Ile Asn
30 35 40

gtc agt gcc ggc acc ttt tat gga att atg ttt gat gcg ggc agc act 375
Val Ser Ala Gly Thr Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr
45 50 55

gga gct cggtt cat gtt tac act ttt gtg cag aaa aca gca gga cag 423
Gly Ala Arg Ile His Val Tyr Thr Phe Val Gln Lys Thr Ala Gly Gln
60 65 70

ctc ccc ttt ctg gaa ggt gaa att ttt gat tct gtg aag ccg gga ctt 471
Leu Pro Phe Leu Glu Gly Ile Phe Asp Ser Val Lys Pro Gly Leu
75 80 85

tct gct ttt gtg gat cag ccc aaa cag ggt gct gag act gtc cag gag 519
Ser Ala Phe Val Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Glu
90 95 100 105

ctc ttg gag gtg gcc aaa gac tcg atc ccc aga agc cac tgg gaa agg		567	
Leu Leu Glu Val Ala Lys Asp Ser Ile Pro Arg Ser His Trp Glu Arg			
110	115	120	
acc ccg gtg gtt ctg aaa gca acg gcc gga ctc cgt ttg ctg cct gag		615	
Thr Pro Val Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu			
125	130	135	
cag aaa gcc cag gct ctg ctc ttg gag gta gag gag atc ttc aag aat		663	
Gln Lys Ala Gln Ala Leu Leu Glu Val Glu Ile Phe Lys Asn			
140	145	150	
tca cct ttc ctg gtc cca gat ggc agc gtt agc atc atg gat ggg tcc		711	
Ser Pro Phe Leu Val Pro Asp Gly Ser Val Ser Ile Met Asp Gly Ser			
155	160	165	
tat gaa ggc ata cta gcc tgg gtt acc gtg aac ttt cta aca ggt cag		759	
Tyr Glu Gly Ile Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln			
170	175	180	185
ctg cat ggt cgt ggc cag gag act gtg ggg acc ctt gac ctg ggg ggt		807	
Leu His Gly Arg Gly Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly			
190	195	200	
gcc tcc acc caa atc acg ttt cta ccc cag ttt gag aaa acc ctg gaa		855	
Ala Ser Thr Gln Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu			
205	210	215	
caa aca cct agg ggc tac ctc act tcc ttt gag atg ttt aac agc act		903	
Gln Thr Pro Arg Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr			
220	225	230	
ttt aag ctc tat aca cat agt tac ttg gga ttt gga ctg aaa gct gca		951	
Phe Lys Leu Tyr Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala			
235	240	245	
aga ctg gca act ctg gga gcc ctg gaa gca aaa ggg act gat gga cat		999	
Arg Leu Ala Thr Leu Gly Ala Leu Glu Ala Lys Gly Thr Asp Gly His			
250	255	260	265
acg ttt cga agt gcc tgt tta cca aga tgg ttg gaa gca gag tgg atc		1047	
Thr Phe Arg Ser Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile			
270	275	280	
ttt ggg ggt gtg aaa tac cag tat ggt ggt aac caa gaa ggg gag atg		1095	
Phe Gly Gly Val Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Met			
285	290	295	
ggc ttt gaa ccc tgc tat gcg gaa gtg ctg agg gta gta cag ggg aaa		1143	
Gly Phe Glu Pro Cys Tyr Ala Glu Val Leu Arg Val Val Gln Gly Lys			
300	305	310	
ctt cac cag cca gaa gaa gtc cga gga agc gcc ttc tac gct ttc tct		1191	
Leu His Gln Pro Glu Glu Val Arg Gly Ser Ala Phe Tyr Ala Phe Ser			
315	320	325	

tac tac tac gat cga gcc gct gac aca cac ttg atc gat tat gaa aag		1239
Tyr Tyr Tyr Asp Arg Ala Ala Asp Thr His Leu Ile Asp Tyr Glu Lys		
330 335	340	345
ggc ggg gtt tta aaa gtt gaa gat ttt gaa aga aaa gcc aga gaa gtg		1287
Gly Gly Val Leu Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val		
350	355	360
tgt gac aac ttg ggg agc ttc tcc tcg ggc agt cct ttc ctc tgc atg		1335
Cys Asp Asn Leu Gly Ser Phe Ser Ser Gly Ser Pro Phe Leu Cys Met		
365	370	375
gac ctc act tac atc aca gcc ctg ttg aaa gat ggt ttg ggc ttt gcc		1383
Asp Leu Thr Tyr Ile Thr Ala Leu Leu Lys Asp Gly Leu Gly Phe Ala		
380	385	390
gaa cgg cac cct ctt aca gct cac aaa gaa agt gaa caa cat aga gac		1431
Glu Arg His Pro Leu Thr Ala His Lys Glu Ser Glu Gln His Arg Asp		
395	400	405
tgg ttg ggc ctt ggg ggc cac ctt tca cct gct cca gtc tct ggg cat		1479
Trp Leu Gly Leu Gly His Leu Ser Pro Ala Pro Val Ser Gly His		
410 415	420	425
cac cag ctg agg cca agc tcc acc tct gaa gcc tgc att tct gaa cca		1527
His Gln Leu Arg Pro Ser Ser Thr Ser Glu Ala Cys Ile Ser Glu Pro		
430	435	440
gtt ttc tca cag gaa ggc gtg gac tca gag aca ttt tct gac ctc tct		1575
Val Phe Ser Gln Glu Gly Val Asp Ser Glu Thr Phe Ser Asp Leu Ser		
445	450	455
gga aaa gcc tgg ccc gaa acc cgt taactggttt tataaggagg gaggggtttt		1629
Gly Lys Ala Trp Pro Glu Thr Arg		
460	465	
tagatgagtc ttgctttga gcctagtat ttggcattca atgatttgca catctaattgt		1689
gaatacgctcc taaccacttg gtgggtgcatt ggctggcacc agactgtaaa tctttggga		1749
ttctttgtac agagtcctgc aaaggaaaaa agagaaaaagg tttggaaactc catgcttagat		1809
tgcgagttca gagacaggc cctggggacc aaagaacaat ctcgtttcaa cccttggatg		1869
cctcattgtt ttgaatggat tcattttgc ttataagctg atttactgaa atcccataac		1929
ccatcaatgc tgttaatttt ttttttcca cccttattac attccctacc ctaaaagcct		1989
gggggaaata cctggtttg cttccatct ataattgaga aagagggggg aaaagatact		2049
gtattagaat ttgtgtgatc ctgtggcaca atagatcaac caaccattt aaagcttaaa		2109
aaaaaaaaaaaa		2119

<210> 8
<211> 465
<212> PRT

<213> Mus musculus

<400> 8
Met Ala Thr Ser Trp Gly Ala Val Phe Met Leu Ile Ile Ala Cys Val
1 5 10 15

Gly Ser Thr Val Phe Tyr Arg Glu Gln Gln Thr Trp Phe Glu Gly Val
20 25 30

Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Gly Thr Phe Tyr
35 40 45

Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Ala Arg Ile His Val Tyr
50 55 60

Thr Phe Val Gln Lys Thr Ala Gly Gln Leu Pro Phe Leu Glu Gly Glu
65 70 75 80

Ile Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln Pro
85 90 95

Lys Gln Gly Ala Glu Thr Val Gln Glu Leu Leu Glu Val Ala Lys Asp
100 105 110

Ser Ile Pro Arg Ser His Trp Glu Arg Thr Pro Val Val Leu Lys Ala
115 120 125

Thr Ala Gly Leu Arg Leu Leu Pro Glu Gln Lys Ala Gln Ala Leu Leu
130 135 140

Leu Glu Val Glu Glu Ile Phe Lys Asn Ser Pro Phe Leu Val Pro Asp
145 150 155 160

Gly Ser Val Ser Ile Met Asp Gly Ser Tyr Glu Gly Ile Leu Ala Trp
165 170 175

Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly Arg Gly Gln Glu
180 185 190

Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr Phe
195 200 205

Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr Leu
210 215 220

Thr Ser Phe Glu Met Phe Asn Ser Thr Phe Lys Leu Tyr Thr His Ser
225 230 235 240

Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly Ala
245 250 255

Leu Glu Ala Lys Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys Leu
260 265 270

Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr Gln
275 280 285

Tyr Gly Gly Asn Gln Glu Gly Glu Met Gly Phe Glu Pro Cys Tyr Ala
 290 295 300
 Glu Val Leu Arg Val Val Gln Gly Lys Leu His Gln Pro Glu Glu Val
 305 310 315 320
 Arg Gly Ser Ala Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala Ala
 325 330 335
 Asp Thr His Leu Ile Asp Tyr Glu Lys Gly Gly Val Leu Lys Val Glu
 340 345 350
 Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Gly Ser Phe
 355 360 365
 Ser Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Thr Tyr Ile Thr Ala
 370 375 380
 Leu Leu Lys Asp Gly Leu Gly Phe Ala Glu Arg His Pro Leu Thr Ala
 385 390 395 400
 His Lys Glu Ser Glu Gln His Arg Asp Trp Leu Gly Leu Gly Gly His
 405 410 415
 Leu Ser Pro Ala Pro Val Ser Gly His His Gln Leu Arg Pro Ser Ser
 420 425 430
 Thr Ser Glu Ala Cys Ile Ser Glu Pro Val Phe Ser Gln Glu Gly Val
 435 440 445
 Asp Ser Glu Thr Phe Ser Asp Leu Ser Gly Lys Ala Trp Pro Glu Thr
 450 455 460
Arg
 465

 <210> 9
 <211> 428
 <212> PRT
 <213> Homo sapiens

 <400> 9
 Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys
 1 5 10 15
 Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
 20 25 30
 Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
 35 40 45
 Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
 50 55 60
 Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
 65 70 75 80

Glu	Val	Phe	Asp	Ser	Val	Lys	Pro	Gly	Leu	Ser	Ala	Phe	Val	Asp	Gln
					85				90					95	
Pro	Lys	Gln	Gly	Ala	Glu	Thr	Val	Gln	Gly	Leu	Leu	Glu	Val	Ala	Lys
					100			105				110			
Asp	Ser	Ile	Pro	Arg	Ser	His	Trp	Lys	Lys	Thr	Pro	Val	Val	Leu	Lys
					115			120				125			
Ala	Thr	Ala	Gly	Leu	Arg	Leu	Leu	Pro	Glu	His	Lys	Ala	Lys	Ala	Leu
					130			135			140				
Leu	Phe	Glu	Val	Lys	Glu	Ile	Phe	Arg	Lys	Ser	Pro	Phe	Leu	Val	Pro
					145			150			155			160	
Lys	Gly	Ser	Val	Ser	Ile	Met	Asp	Gly	Ser	Asp	Glu	Gly	Ile	Leu	Ala
					165			170				175			
Trp	Val	Thr	Val	Asn	Phe	Leu	Thr	Gly	Gln	Leu	His	Gly	His	Arg	Gln
					180			185			190				
Glu	Thr	Val	Gly	Thr	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Ile	Thr
					195			200			205				
Phe	Leu	Pro	Gln	Phe	Glu	Lys	Thr	Leu	Glu	Gln	Thr	Pro	Arg	Gly	Tyr
					210			215			220				
Leu	Thr	Ser	Phe	Glu	Met	Phe	Asn	Ser	Thr	Tyr	Lys	Leu	Tyr	Thr	His
					225			230			235			240	
Ser	Tyr	Leu	Gly	Phe	Gly	Leu	Lys	Ala	Ala	Arg	Leu	Ala	Thr	Leu	Gly
					245			250			255				
Ala	Leu	Glu	Thr	Glu	Gly	Thr	Asp	Gly	His	Thr	Phe	Arg	Ser	Ala	Cys
					260			265			270				
Leu	Pro	Arg	Trp	Leu	Glu	Ala	Glu	Trp	Ile	Phe	Gly	Gly	Val	Lys	Tyr
					275			280			285				
Gln	Tyr	Gly	Gly	Asn	Gln	Glu	Gly	Glu	Val	Gly	Phe	Glu	Pro	Cys	Tyr
					290			295			300				
Ala	Glu	Val	Leu	Arg	Val	Val	Arg	Gly	Lys	Leu	His	Gln	Pro	Glu	Glu
					305			310			315			320	
Val	Gln	Arg	Gly	Ser	Phe	Tyr	Ala	Phe	Ser	Tyr	Tyr	Tyr	Asp	Arg	Ala
					325			330			335				
Val	Asp	Thr	Asp	Met	Ile	Asp	Tyr	Glu	Lys	Gly	Gly	Ile	Leu	Lys	Val
					340			345			350				
Glu	Asp	Phe	Glu	Arg	Lys	Ala	Arg	Glu	Val	Cys	Asp	Asn	Leu	Glu	Asn
					355			360			365				
Phe	Thr	Ser	Gly	Ser	Pro	Phe	Leu	Cys	Met	Asp	Leu	Ser	Tyr	Ile	Thr
					370			375			380				

Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
385 390 395 400

Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala
405 410 415

Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
420 425

<210> 10
<211> 455
<212> PRT
<213> P. sativum

<400> 10
Met Glu Leu Leu Ile Lys Leu Ile Thr Phe Leu Leu Phe Ser Met Pro
1 5 10 15

Ala Ile Thr Ser Ser Gln Tyr Leu Gly Asn Asn Leu Leu Thr Ser Arg
20 25 30

Lys Ile Phe Leu Lys Gln Glu Glu Ile Ser Ser Tyr Ala Val Val Phe
35 40 45

Asp Ala Gly Ser Thr Gly Ser Arg Ile His Val Tyr His Phe Asn Gln
50 55 60

Asn Leu Asp Leu Leu His Ile Gly Lys Gly Val Glu Tyr Tyr Asn Lys
65 70 75 80

Ile Thr Pro Gly Leu Ser Ser Tyr Ala Asn Asn Pro Glu Gln Ala Ala
85 90 95

Lys Ser Leu Ile Pro Leu Leu Glu Gln Ala Glu Asp Val Val Pro Asp
100 105 110

Asp Leu Gln Pro Lys Thr Pro Val Arg Leu Gly Ala Thr Ala Gly Leu
115 120 125

Arg Leu Leu Asn Gly Asp Ala Ser Glu Lys Ile Leu Gln Ser Val Arg
130 135 140

Asp Met Leu Ser Asn Arg Ser Thr Phe Asn Val Gln Pro Asp Ala Val
145 150 155 160

Ser Ile Ile Asp Gly Thr Gln Glu Gly Ser Tyr Leu Trp Val Thr Val
165 170 175

Asn Tyr Ala Leu Gly Asn Leu Gly Lys Lys Tyr Thr Lys Thr Val Gly
180 185 190

Val Ile Asp Leu Gly Gly Ser Val Gln Met Ala Tyr Ala Val Ser
195 200 205

Lys Lys Thr Ala Lys Asn Ala Pro Lys Val Ala Asp Gly Asp Asp Pro
210 215 220

Tyr Ile Lys Lys Val Val Leu Lys Gly Ile Pro Tyr Asp Leu Tyr Val
 225 230 235 240
 His Ser Tyr Leu His Phe Gly Arg Glu Ala Ser Arg Ala Glu Ile Leu
 245 250 255
 Lys Leu Thr Pro Arg Ser Pro Asn Pro Cys Leu Leu Ala Gly Phe Asn
 260 265 270
 Gly Ile Tyr Thr Tyr Ser Gly Glu Glu Phe Lys Ala Thr Ala Tyr Thr
 275 280 285
 Ser Gly Ala Asn Phe Asn Lys Cys Lys Asn Thr Ile Arg Lys Ala Leu
 290 295 300
 Lys Leu Asn Tyr Pro Cys Pro Tyr Gln Asn Cys Thr Phe Gly Gly Ile
 305 310 315 320
 Trp Asn Gly Gly Asn Gly Gln Lys Asn Leu Phe Ala Ser Ser
 325 330 335
 Ser Phe Phe Tyr Leu Pro Glu Asp Thr Gly Met Val Asp Ala Ser Thr
 340 345 350
 Pro Asn Phe Ile Leu Arg Pro Val Asp Ile Glu Thr Lys Ala Lys Glu
 355 360 365
 Ala Cys Ala Leu Asn Phe Glu Asp Ala Lys Ser Thr Tyr Pro Phe Leu
 370 375 380
 Asp Lys Lys Asn Val Ala Ser Tyr Val Cys Met Asp Leu Ile Tyr Gln
 385 390 395 400
 Tyr Val Leu Leu Val Asp Gly Phe Gly Leu Asp Pro Leu Gln Lys Ile
 405 410 415
 Thr Ser Gly Lys Glu Ile Glu Tyr Gln Asp Ala Ile Val Glu Ala Ala
 420 425 430
 Trp Pro Leu Gly Asn Ala Val Glu Ala Ile Ser Ala Leu Pro Lys Phe
 435 440 445
 Glu Arg Leu Met Tyr Phe Val
 450 455

 <210> 11
 <211> 454
 <212> PRT
 <213> Solanum tuberosum

 <400> 11
 Met Leu Asn Gln Asn Ser His Phe Ile Phe Ile Ile Leu Ala Ile Phe
 1 5 10 15
 Leu Val Leu Pro Leu Ser Leu Leu Ser Lys Asn Val Asn Ala Gln Ile
 20 25 30

Pro Leu Arg Arg His Leu Leu Ser His Glu Ser Glu His Tyr Ala Val
 35 40 45

 Ile Phe Asp Ala Gly Ser Thr Gly Ser Arg Val His Val Phe Arg Phe
 50 55 60

 Asp Glu Lys Leu Gly Leu Leu Pro Ile Gly Asn Asn Ile Glu Tyr Phe
 65 70 75 80

 Met Ala Thr Glu Pro Gly Leu Ser Ser Tyr Ala Glu Asp Pro Lys Ala
 85 90 95

 Ala Ala Asn Ser Leu Glu Pro Leu Leu Asp Gly Ala Glu Gly Val Val
 100 105 110

 Pro Gln Glu Leu Gln Ser Glu Thr Pro Leu Glu Leu Gly Ala Thr Ala
 115 120 125

 Gly Leu Arg Met Leu Lys Gly Asp Ala Ala Glu Lys Ile Leu Gln Ala
 130 135 140

 Val Arg Asn Leu Val Lys Asn Gln Ser Thr Phe His Ser Lys Asp Gln
 145 150 155 160

 Trp Val Thr Ile Leu Asp Gly Thr Gln Glu Gly Ser Tyr Met Trp Ala
 165 170 175

 Ala Ile Asn Tyr Leu Leu Gly Asn Leu Gly Lys Asp Tyr Lys Ser Thr
 180 185 190

 Thr Ala Thr Ile Asp Leu Gly Gly Ser Val Gln Met Ala Tyr Ala
 195 200 205

 Ile Ser Asn Glu Gln Phe Ala Lys Ala Pro Gln Asn Glu Asp Gly Glu
 210 215 220

 Pro Tyr Val Gln Gln Lys His Leu Met Ser Lys Asp Tyr Asn Leu Tyr
 225 230 235 240

 Val His Ser Tyr Leu Asn Tyr Gly Gln Leu Ala Gly Arg Ala Glu Ile
 245 250 255

 Phe Lys Ala Ser Arg Asn Glu Ser Asn Pro Cys Ala Leu Glu Gly Cys
 260 265 270

 Asp Gly Tyr Tyr Ser Tyr Gly Gly Val Asp Tyr Lys Val Lys Ala Pro
 275 280 285

 Lys Lys Gly Ser Ser Trp Lys Arg Cys Arg Arg Leu Thr Arg His Ala
 290 295 300

 Leu Lys Ile Asn Ala Lys Cys Asn Ile Glu Glu Cys Thr Phe Asn Gly
 305 310 315 320

 Val Trp Asn Gly Gly Gly Asp Gly Gln Lys Asn Ile His Ala Ser
 325 330 335

Ser Phe Phe Tyr Asp Ile Gly Ala Gln Val Gly Ile Val Asp Thr Lys
 340 345 350

 Phe Pro Ser Ala Leu Ala Lys Pro Ile Gln Tyr Leu Asn Ala Ala Lys
 355 360 365

 Val Ala Cys Gln Thr Asn Val Ala Asp Ile Lys Ser Ile Phe Pro Lys
 370 375 380

 Thr Gln Asp Arg Asn Ile Pro Tyr Leu Cys Met Asp Leu Ile Tyr Glu
 385 390 395 400

 Tyr Thr Leu Leu Val Asp Gly Phe Gly Leu Asn Pro His Lys Glu Ile
 405 410 415

 Thr Val Ile His Asp Val Gln Tyr Lys Asn Tyr Leu Val Gly Ala Ala
 420 425 430

 Trp Pro Leu Gly Cys Ala Ile Asp Leu Val Ser Ser Thr Thr Asn Lys
 435 440 445

 Ile Arg Val Ala Ser Ser
 450

 <210> 12
 <211> 473
 <212> PRT
 <213> *Saccharomyces cerevisiae*

 <400> 12
 Lys Thr Pro Glu Asp Ile Ser Ile Ile Pro Val Asn Asp Glu Pro Gly
 1 5 10 15

 Tyr Leu Gln Asp Ser Lys Thr Glu Gln Asn Tyr Pro Glu Leu Ala Asp
 20 25 30

 Ala Val Lys Ser Gln Thr Ser Gln Thr Cys Ser Glu Glu His Lys Tyr
 35 40 45

 Val Ile Met Ile Asp Ala Gly Ser Thr Gly Ser Arg Val His Ile Tyr
 50 55 60

 Lys Phe Asp Val Cys Thr Ser Pro Pro Thr Leu Leu Asp Glu Lys Phe
 65 70 75 80

 Asp Met Leu Glu Pro Gly Leu Ser Ser Phe Asp Thr Asp Ser Val Gly
 85 90 95

 Ala Ala Asn Ser Leu Asp Pro Leu Leu Lys Val Ala Met Asn Tyr Val
 100 105 110

 Pro Ile Lys Ala Arg Ser Cys Thr Pro Val Ala Val Lys Ala Thr Ala
 115 120 125

 Gly Leu Arg Leu Leu Gly Asp Ala Lys Ser Ser Lys Ile Leu Ser Ala
 130 135 140

Val Arg Asp His Leu Glu Lys Asp Tyr Pro Phe Pro Val Val Glu Gly
 145 150 155 160
 Asp Gly Val Ser Ile Met Gly Gly Asp Glu Glu Gly Val Phe Ala Trp
 165 170 175
 Ile Thr Thr Asn Tyr Leu Leu Gly Asn Ile Gly Ala Asn Gly Pro Lys
 180 185 190
 Leu Pro Thr Ala Ala Val Phe Asp Leu Gly Gly Ser Thr Gln Ile
 195 200 205
 Val Glu Glu Pro Thr Phe Pro Ile Asn Glu Lys Met Val Asp Gly Glu
 210 215 220
 His Lys Phe Asp Leu Lys Phe Gly Asp Glu Asn Tyr Thr Leu Tyr Gln
 225 230 235 240
 Phe Ser His Leu Gly Tyr Gly Leu Lys Glu Gly Arg Asn Lys Val Asn
 245 250 255
 Ser Val Leu Val Glu Asn Ala Leu Lys Asp Lys Ile Leu Lys Gly Cys
 260 265 270
 Asn Thr Lys Thr His Cys Leu Ser Ser Pro Cys Leu Pro Pro Lys Val
 275 280 285
 Asn Ala Thr Asn Glu Lys Val Thr Leu Glu Ser Lys Glu Thr Tyr Thr
 290 295 300
 Ile Asp Phe Ile Gly Pro Asp Glu Pro Ser Gly Ala Gln Cys Arg Phe
 305 310 315 320
 Leu Thr Asp Glu Ile Leu Asn Lys Asp Ala Gln Cys Gln Ser Pro Pro
 325 330 335
 Cys Ser Phe Asn Gly Val His Gln Pro Ser Leu Val Arg Thr Phe Lys
 340 345 350
 Glu Ser Asn Asp Ile Tyr Ile Phe Ser Tyr Phe Tyr Asp Arg Thr Thr
 355 360 365
 Arg Pro Leu Gly Met Pro Leu Ser Phe Thr Leu Asn Glu Leu Asn Asp
 370 375 380
 Leu Ala Arg Ile Val Cys Lys Gly Glu Glu Thr Trp Asn Ser Val Phe
 385 390 , 395 400
 Ser Gly Ile Ala Gly Ser Leu Asp Glu Leu Glu Ser Asp Ser His Phe
 405 410 415
 Cys Leu Asp Leu Ser Phe Gln Val Ser Leu Leu His Thr Gly Tyr Asp
 420 425 430
 Ile Pro Leu Gln Arg Glu Leu Arg Thr Gly Lys Lys Ile Ala Asn Lys
 435 440 445

Glu Ile Gly Trp Cys Leu Gly Ala Ser Leu Pro Leu Leu Lys Ala Asp
450 455 460

Asn Trp Lys Cys Lys Ile Gln Ser Ala
465 470

<210> 13
<211> 153
<212> PRT
<213> Homo sapiens

<400> 13
Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr
1 5 10 15

Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His
20 25 30

Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val
35 40 45

Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg
50 55 60

Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr
65 70 75 80

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu
85 90 95

Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr
100 105 110

Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly
115 120 125

Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln
130 135 140

Lys Thr Arg Trp Phe Ser Ile Val Pro
145 150

<210> 14
<211> 154
<212> PRT
<213> Rattus norvegicus

<400> 14
Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Asn Leu
1 5 10 15

Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
20 25 30

Gln Leu Leu Glu Glu Cys Gln Val Lys Gly Pro Gly Ile Ser Lys Tyr
35 40 45

Ala Gln Lys Thr Asp Glu Ile Ala Ala Tyr Leu Ala Glu Cys Met Lys
50 55 60

Met Ser Thr Glu Arg Ile Pro Ala Ser Lys Gln His Gln Thr Pro Val
65 70 75 80

Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Lys
85 90 95

Gln Ser Ala Asp Glu Val Leu Ala Ala Val Ser Arg Ser Leu Lys Ser
100 105 110

Tyr Pro Phe Asp Phe Gln Gly Ala Lys Ile Ile Thr Gly Gln Glu Glu
115 120 125

Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Arg Phe Thr
130 135 140

Gln Glu Gln Ser Trp Leu Asn Phe Ile Ser
145 150

<210> 15
<211> 153
<212> PRT
<213> Homo sapiens

<400> 15
Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Met Phe
1 5 10 15

Ile Tyr Lys Trp Pro Ala Asp Lys Glu Asn Asp Thr Gly Ile Val Gly
20 25 30

Gln His Ser Ser Cys Asp Val Pro Gly Gly Ile Ser Ser Tyr Ala
35 40 45

Asp Asn Pro Ser Gly Ala Ser Gln Ser Leu Val Gly Cys Leu Glu Gln
50 55 60

Ala Leu Gln Asp Val Pro Lys Glu Arg His Ala Gly Thr Pro Leu Tyr
65 70 75 80

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Asn Leu Thr Asn Pro Glu
85 90 95

Ala Ser Thr Ser Val Leu Met Ala Val Thr His Thr Leu Thr Gln Tyr
100 105 110

Pro Phe Asp Phe Arg Gly Ala Arg Ile Leu Ser Gly Gln Glu Glu Gly
115 120 125

Val Phe Gly Trp Val Thr Ala Asn Tyr Leu Leu Glu Asn Phe Ile Lys
130 135 140

Tyr Gly Trp Val Gly Arg Trp Phe Arg
145 150

<210> 16
 <211> 150
 <212> PRT
 <213> Gallus gallus

<400> 16
 Phe Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ala Val
 1 5 10 15

Phe Ile Tyr Lys Trp Pro Ala Asp Lys Glu Asn Asp Thr Gly Val Val
 20 25 30

Ser Glu His Ser Met Cys Asp Val Glu Gly Pro Gly Ile Ser Ser Tyr
 35 40 45

Ser Ser Lys Pro Pro Ala Ala Gly Lys Ser Leu Glu His Cys Leu Ser
 50 55 60

Gln Ala Met Arg Asp Val Pro Lys Glu Lys His Ala Asp Thr Pro Leu
 65 70 75 80

Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Thr Ile Ala Asp Pro
 85 90 95

Pro Ser Gln Thr Cys Leu Ser Ala Val Met Ala Thr Leu Lys Ser Tyr
 100 105 110

Pro Phe Asp Phe Gly Gly Ala Lys Ile Leu Ser Gly Glu Glu Gly
 115 120 125

Val Phe Gly Trp Ile Thr Ala Asn Tyr Leu Leu Glu Asn Phe Ile Lys
 130 135 140

Arg Gly Trp Leu Gly Glu
 145 150

<210> 17
 <211> 148
 <212> PRT
 <213> Caenorhabditis elegans

<400> 17
 Ile Lys Tyr Gly Val Ile Cys Asp Ala Gly Ser Ser Gly Thr Arg Leu
 1 5 10 15

Phe Val Tyr Thr Leu Lys Pro Leu Ser Gly Gly Leu Thr Asn Ile Asp
 20 25 30

Thr Leu Ile His Glu Ser Glu Pro Val Val Lys Lys Val Thr Pro Gly
 35 40 45

Leu Ser Ser Phe Gly Asp Lys Pro Glu Gln Val Val Glu Tyr Leu Thr
 50 55 60

Pro Leu Leu Arg Phe Ala Glu Glu His Ile Pro Tyr Glu Gln Leu Gly
 65 70 75 80

Glu Thr Asp Leu Leu Ile Phe Ala Thr Ala Gly Met Arg Leu Leu Pro
85 90 95

Glu Ala Gln Lys Asp Ala Ile Ile Lys Asn Leu Gln Asn Gly Leu Lys
100 105 110

Ser Val Thr Ala Leu Arg Val Ser Asp Ser Asn Ile Arg Ile Ile Asp
115 120 125

Gly Ala Trp Glu Gly Ile Tyr Ser Trp Ile Ala Val Asn Tyr Ile Leu
130 135 140

Gly Arg Phe Asp
145

<210> 18
<211> 10
<212> RNA
<213> Mus musculus

<400> 18
aagaauaugg 10

<210> 19
<211> 10
<212> RNA
<213> Vertebrate

<400> 19
gccgcuaagg 10

<210> 20
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 20
ccagactgta aatcttttgg 20

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 21
agggaaatgta ataagggtag 20

20

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 22
ctgcttgagt gacgtctctg

<210> 23
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 23
cacatgaggt tcagtcgtg

<210> 24
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 24
gtgaagtggc tgccttcagg

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
cctttgactc gggactccag

<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 26
gaactgctgc ctaaccactc

<210> 27
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 27
attgatgggt cttgggattg c 21

<210> 28
<211> 10
<212> RNA
<213> Homo sapiens

<400> 28
augugaauga 10

<210> 29
<211> 10
<212> RNA
<213> Homo sapiens

<400> 29
acaaggaua 10